



Insights into the microbiota of the bovine uterus

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Insights into the microbiota of the bovine uterus

Recent years' advance in sequencing technology has resulted in extensive new knowledge of the microbial ecology of different environments. We used the technology to investigate the causality of endometritis, which is an inflammation in the inner lining of the uterus affecting up to 20% of dairy cows in Denmark post partum. Endometritis is linked to reduced reproductive performance, which is costly for the farmer and often leads to culling of the affected cows. With incomplete knowledge of the bacteria involved, treatment is performed without an option for choosing the best suited antimicrobial agent, which may lead to unnecessary antibiotic resistance development. Slaughterhouse samples were analysed in order to obtain information on the uterine microbiota from both cows with endometritis and seemingly healthy cows from a variety of herds.

We sampled uteri from cows (n=50) from a slaughterhouse in Holstebro, Denmark. An incision was made into the right uterine horn and an endometrial biopsy was taken with a pair of sterilised scissors. The endometrial surface was sampled with a cotton-swab through the same incision. All samples were immediately put in RNAlater. The DNA was extracted with the Maxwell 16 LEV Blood kit (Promega), the 16S rRNA PCR was performed with primers targeting the V2 region, and the 454 next generation sequencing was performed by GATC.

Previous results have shown that *Proteobacteria* and *Tenericutes* are the most important bacteria phyla in the uterus of healthy cows (Machado *et al.* 2012 and Galvão *et al.* 2012) while *Escherichia coli*, *Trueperella Pyogenes*, *Prevotella* species and *Fusobacterium necrophorum* have commonly been associated with endometritis (Sheldon 2006). Preliminary results indicate that we often find bacteria from phylum *Actinobacteria* in the healthy cows and often bacteria from phyla *Bacteroidetes* and *Fusobacteria* in cows with endometritis.